Package: FnR (via r-universe)

September 16, 2024

Title Inbreeding and Numerator Relationship Coefficients

Version 1.1.0

Description Compute inbreeding coefficients using the method of
Meuwissen and Luo (1992) <doi:10.1186/1297-9686-24-4-305>, and
numerator relationship coefficients between individuals using
the method of Van Vleck (2007)
<https://pubmed.ncbi.nlm.nih.gov/18050089/>.

License GPL (>= 3)

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.1

Suggests knitr, rmarkdown

VignetteBuilder knitr

URL https://github.com/nilforooshan/FnR

BugReports https://github.com/nilforooshan/FnR/issues

Repository https://nilforooshan.r-universe.dev

RemoteUrl https://github.com/nilforooshan/fnr

RemoteRef HEAD

RemoteSha 7d63f780871748214383cd24d8d6fb1a4721edee

Contents

| calcR | *Compute numerator relationship coefficients between two distinct groups of individuals* |

Description

Compute numerator relationship coefficients between two distinct groups of individuals

Usage

```
calcR(ped, set1, set2, type = "notdam-notsire", f = c(), d = c())
```

Arguments

ped	: A data frame with integer columns corresponding to ID, SIRE, and DAM. IDs should be sequential, starting from 1. Missing parents (SIRE and DAM) are denoted as 0.
set1	: A set of individual IDs.
set2	: A set of individual IDs, distinct from set1.
type	: "notdam-notsire" (default), "sire-sire", or "dam-dam" relationships
	"notdam-notsire" requires set1 and set2 individuals not to be members of ped$DAM and ped$SIRE, respectively.
	"sire-sire" requires set1 and set2 individuals to be members of ped$SIRE.
	"dam-dam" requires set1 and set2 individuals to be members of ped$DAM.
f	: (Optional) If available, the vector of inbreeding coefficients for the whole pedigree (without dummy progeny) or from the previous calculation of inbreeding coefficients with less number of animals in the pedigree.
d	: (Optional) If available, the vector of the diagonal elements of the diagonal matrix $\mathbf{D}$ in $\mathbf{A} = \mathbf{TDT}'$ where $\mathbf{A}$ is the numerator relationship matrix, for the whole pedigree (without dummy progeny) or from the previous calculation of inbreeding coefficients with less number of animals in the pedigree.

Value

: Numerator relationship coefficients between set1 and set2 individuals in the form of a matrix (a partition of the numerator relationship matrix $\mathbf{A}$).

Examples

```
# A sample pedigree data frame:
ped <- data.frame(
    ID = 1:12,
    SIRE = c(0, 0, 0, 2, 2, 0, 4, 6, 0, 6, 10, 10),
    DAM = c(0, 0, 0, 1, 1, 0, 3, 5, 7, 8, 9, 0)
)
```

```
# Example 1: Calculate relationship coefficients between two groups of animals,
# one's members not among dams, and the members of the other not among sires.
calcR(ped, set1 = c(12, 6), set2 = c(11, 8), type = "notdam-notsire")
# Since `"notdam-notsire"` is the default type, `type = "notdam-notsire"` might be omitted.

# Example 2: Calculate relationship coefficients between dam 7 and dams 8 and 9.
calcR(ped, set1 = 7, set2 = 8:9, type = "dam-dam")

# Example 3: Calculate relationship coefficients between sires 2 & 6 and sires 4 & 10.
calcR(ped, set1 = c(2, 6), set2 = c(4, 10), type = "sire-sire")

# Example 5: Repeat example 2 with inbreeding coefficients provided.
f <- rep(0, 12)
f[10] <- 0.25
f[11] <- 0.015625
calcR(ped, set1 = 7, set2 = 8:9, type = "dam-dam", f = f)

# Example 6: Repeat example 3 with inbreeding and d coefficients provided.
d <- c(1, 1, 1, 0.5, 0.5, 1, 0.5, 0.5, 0.75, 0.5, 0.4375, 0.6875)
calcR(ped, set1 = c(2, 6), set2 = c(4, 10), type = "sire-sire", f = f, d = d)
```

---

resume_inbreed	*Calculate inbreeding coefficients from scratch or resume for new individuals in the pedigree*

Description

Calculate inbreeding coefficients from scratch or resume for new individuals in the pedigree

Usage

```
resume_inbreed(ped, f = c(), d = c(), export_d = FALSE)
```

Arguments

ped	: A data frame with integer columns corresponding to ID, SIRE, and DAM. IDs should be sequential, starting from 1. Missing parents (SIRE and DAM) are denoted as 0.
f	: (Optional) If available, the vector of inbreeding coefficients from the previous calculation of inbreeding coefficients with less number of animals in the pedigree.
d	: (Optional) If available, the vector of the diagonal elements of the diagonal matrix $\mathbf{D}$ in $\mathbf{A} = \mathbf{TDT}'$ from the previous calculation of inbreeding coefficients with less number of animals in the pedigree, where $\mathbf{A}$ is the numerator relationship matrix.
export_d	: FALSE (default) or TRUE. If TRUE, vector d is retuned for future use.

Value

: Vector of inbreeding coefficients if `export_d == FALSE`, or a list containing the vector of inbreeding coefficients and the vector of d coefficients if `export_d == TRUE`.

Examples

```
# A sample pedigree data frame:
ped <- data.frame(
    ID = 1:12,
    SIRE = c(0, 0, 0, 2, 2, 0, 4, 6, 0, 6, 10, 10),
    DAM = c(0, 0, 0, 1, 1, 0, 3, 5, 7, 8, 9, 0)
)

oldped <- ped[1:9, ]
(oldrun <- resume_inbreed(oldped, export_d = TRUE))
resume_inbreed(ped)
resume_inbreed(ped, f = oldrun$f)
resume_inbreed(ped, f = oldrun$f, d = oldrun$d)
```

Index